In the specification:

Please amend paragraph [0005] as follows:

[0005] NKCC1 (the sequence of which can be found under the accession number P55011 in the SwissProt database, ~~(available at http://www.expasy.org/),~~ and which is shown in FIG. 1, SEQ ID NO:1) is a bumetanide sensitive sodium-potassium-chloride (Na--K--Cl) cotransporter (Payne et al, 1995, J Biol Chem, 270(30): pp 17977-17985). Two isoforms of the Na--K--Cl cotransporter have been identified; one located on the apical membrane of absorptive epithelia (NKCC2) and one located on the basolateral membrane of secretory epithelia (NKCC1). The function of the Na--K--Cl cotransporters is to provide electroneutral transport of chloride ions across epithelia (in a ratio of 1Na: 1K:2Cl), they work in combination with the sodium and potassium channels and the sodium pump to cause a net transport of sodium chloride across membranes. Dysregulation of this transport mechanism can result in diseases such as Cystic Fibrosis and secretory diarrhoea.

Please amend paragraph [0210] as follows:

[0210] FIG. 1: shows the nucleotide and amino acid sequences of NKCC1 (SEQ ID NO: 1; GenBank accession: U30246; SwissProt accession: P55011). The tandem spectra used to identify NKCC1 in breast and pancreatic cancer cell line membrane preparations are shown in bold, italicised, and underlined. Masses assigned to NKCC1 are shown in bold and italicised (see below).

Please amend paragraph [0219] as follows:

[0219] Using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976 989), uninterpreted tandem mass spectra of tryptic digest peptides were searched against a database of public domain proteins constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI). ~~This database is accessible at http://www.ncbi.nlm.nih.gov/ and also constructed of Expressed Sequence Tags entries (http://www.ncbi.nlm.nih.gov/dbEST/index.html).~~

As a result of sequence database searching tandem amino acid sequences were found to match a SwissProt accession number: P55011 (Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 1), see FIG. 1 (SEQ ID NO: 1), matched tandem sequences are shown in bold.

Please amend paragraph [0220] as follows:

[0220] Additionally, sequences were identified using peptide mass data derived from mass spectrometer analysis and the MOWSE database search procedure. Peptide mass information can provide a `fingerprint` signature sufficiently discriminating to allow for the unique and rapid identification of unknown sample proteins, independent of other analytical methods such as protein sequence analysis. Practical experience has shown that sample proteins can be uniquely identified using as few as 3-4 experimentally determined peptide masses when screened against a fragment database derived from over 50,000 proteins (D. J. C. Pappin, P. Hojrup and A. J. Bleasby `Rapid Identification of Proteins by Peptide-Mass Fingerprinting`. Current Biology (1993), vol 3, 327-332. ~~and http://www.hgmp.mrc.ac.uk/Bioinformatics/Webapp/mowse/~~). The version of the code used for a MOWSE database search had the following modifications: the size of the parent protein is not included in the calculation such that large proteins such as titin no longer bias the score; instead the theoretical frequency of a peptide of mass (x) is estimated using the mass (x) of the peptide and the mean mass of an amino acid whilst allowing for a probability of 0.2 for a missed internal cleavage (by trypsin) and 0.1 for the probability of the occurrence of a proteolytic cleavage site.